

1 MAODSSPKORPCGCTFNNATETWYTHDPDPTPCPEQATLVNTPGAFYNAPFVLFDPYLLKASLDNRNIPWKNXLMVSKALVNLGLLVITALDLIMALVKKG-GDSELPFLYDLDVWGPI
MALRGFC--SADGSDPLNDNNVTWNTSNPDFTKCFQNTVLVNVPCFYLNACPPFYFLYLSHRDRCYIQHTPLNKTATGCLFLEMLVWCWADLFBYBTHRSRGIFLAFPLVLS--P
116 IKFATPLLLPIFILNKKYGVQPTGCFIPWPLLTULSIPRCRTHVRLDAROKILNSQOSEQDFSNERYQVSPFIPPTFTSMLLLNCFADHMPRQTKYQRCGEHPIBELSASF
LLGITHLLATELLOERRKGVQSSGINTLFWLVALVCAILAKSKIMTALKEQADVD-----LPRDTTFYVYFSLTIQVLVLSCEFSDRSLPSETIHOPPCPSSASP
232 LSRITQWPKMAKCYRNPLEEKDLDWDLRPODSCSEVMPIFAMHWNQNVKNYK-----NKARVERPKAOFSGMGNVTFZFNPHGEKNGRKKMGMASIMPPYIKKSPGCVFLTFGALH
LSRIFENWITGLIVGCVROPLEGSDLSLNKEEDTSRQVVPVLVKNKKCEKAKTKQPKVVPVSSXDPAPQPKRSSKVDANEVEALVKSPOKEHNSLSFKVLKYTKTFGTFYELMBFFE
340 KLPTDTLTPAQPOVLSLJISFVERAQDARFENKCILYAVULLFVLAAAOFTLGOYFPHMFIVGLRIRRTALIMAYRKAALRISMTSESTVGTIUNLMAVDAQORPMELTYLNMIMS
KAIHDLNMFSGPQILKLLIKFVNDTXAP-DWQGYFYTVLLFVTAQTLVLNKHQPHICFPVSGNRIKTAVIGAVYRKAALVITNSAKRSSTVGEIVNLSKSVDAQORPHDLARYIMIMS
456 APLQIGLALYFLNQOLGSPVLAGLAVMIILIPVNGVIASRIKTYQIRONKXKDERVKLMNREVLSGIKVLKLYAMHPSPEKQVLDERDKEIATLRSFAYLNAGTSPLMSCAPFLVSL
APLQVTLALYLLMLLGLSPVLAGVAVNLMVPPVNAVMAKTKTYQVAHNSKXDNRIKLMHREILNGIKVLELYAWELAFKDKVLAIKQBELXVLKKSAYLSAVGTPTTWVCTPFFLVAL
572 VIFATYVLIDEMHVLDAKTPVSLSLPFXILRPLTLNPLMLITLVLQTVQSVNRIKXFLNSELDPNSVLMDSKPR--PMSIRNQEFSWC--DEITLRNINIEVKKESLVALVG
CITFAYVUTIDERHNLDAQATAPVSLALFPLRPLNINLBNVISSIVQSVSLKRLAIRFLSHSELEPDSIERRPVROGGGTNSITVBNATPTMARSDPTTNGITFTFTSECALVAVVQ
682 TVGSGKSSUVQAFGEHREKLACGVNTEVCKLAYVPPQAMIQONATVRDMLPGQTYDRKRYNKVIDACALRADIDILSAOLTEIGCKINLSGGKORLSLARA VYSDADLYLDDPL
QVCGCRSSLALTAEMDKVECHVAIKGSVAYVPPQAMIQONDSIREMILPGCQLEEFYYSVIOACALLPDLBILPESDRTEIGERGVNLSGQKQKRVSLARAVYSNADITLDPDPL
798 SAYDAHVGRHIFERVIKPKGILARKSRVLVTHGVTFPLQVDSIYVIMKCEIASEGTFDQVLVKNKGAFADGEIIONLQEGNKECEELQIKRROISSTADVPPELLGTVKAKLARTB
SAVDAHVCKHIFENVICPKGMLKKNKTRILVTHBSMSYLPQVDVIVMSGKXISEMGSYQELLARDCAFAEGFLRTYASTEQEODARENGVTVGSGPGKXAKOMENGHL-----
914 SLSDSISVTSADSLKCGGSLRRRTKRODSKOSVASASLXKKQZVEG--KLIRTEKXSGCVPEFAVYKHYIKSVGIFLSVATLVNPFVQAFQIGSNLMLTQMANQONVANDTGL
-VTDSACKQLQROLSSESSYSYSGDISR-----HRNSTAFELQAEAKKEBFWKLMHEADKAQTOQVXLSVYWDYHKKITGLFISPLSIFPMCNHVSALASWYLSLMTDDPIVNGTQEH
1028 ROKYLCVYGPFOPCQVLSYLSGLLAIQGLGCSNMUPMELLMTGEMPHLPTDTPLCRILBRYSKDDTUDSVLPATVOLLKTCPOVLATIVVISLSTPIFLAVIVPLAPLXY
TKVLSVYVYALGALGISOCTIAVFGYSMAVSIIGCILASRCUNVDELHSHILRSNPSFFEXTPSGNLVNRPFSKELDTVDSNIPFVIXMFMGSCFNVIACIVILLATPIAAIYIPPLCLIYF
1144 FAORFYVATSRQMLNLESVSRBPYXSHPSFTVTGASTIRAYNVGDXPIESDARVDXMQVCKYFSPVLANNWLAIRLXNVGNLIILFASLEFVLG-GQTFPGLVGLSVSYALQVTOE
PVORFYVASSHQLKRLSVSRSPVISHFETLLGVSUTRAFEQEERFIHQSLKVDEHQXAYYFYSIVANNWLAVALCEVGNCAIVTFAALFAVISRBSLSAGLVGLSVSYSLQVTTY
1259 LNWLVNMSSEHETHIVAVBRALXBYSETEKEAPWQIQE-TAPPSSWFOVGHVERFHYCLRTREDDLPVLEHINVTINGGEEKVUGIVGTGAGKSSLLTGLTFAINBSABOETITDGINI
LNWLVNMSSEHETHIVAVBRALXBYSETEKEAPWQIQE-TAPPSSWFOVGHVERFHYCLRTREDDLPVLEHINVTINGGEEKVUGIVGTGAGKSSLLTGLTFAINBSABOETITDGINI
1375 ASKGLNLSRSLTIPODPVLPFGSLRINLDPPEIKTDDDEIMKALELSLXKSPVKSLSAAGLMBEJAEGBEPLSGOROLVCLARLARKTKRVLDHATAAVDLEETODLIQATIR
AXYGLHDLNPKTITIPQDPVLPFGSLRINLDPPEIKTDDDEIMKALELSLXKSPVKSLSAAGLMBEJAEGBEPLSGOROLVCLARLARKTKRVLDHATAAVDLEETODLIQATIR
1491 EPRACETVLTIAHALNITLDSKXVIVLDKQOIEFAPETELLDNPKXSAFYSHAKOANLV
QPEDCTVLTIAHALNITINDYTRVIVLDKGEIOEYCAPSOLLQOR-GLFYSHAKDAGLV

Figure 1

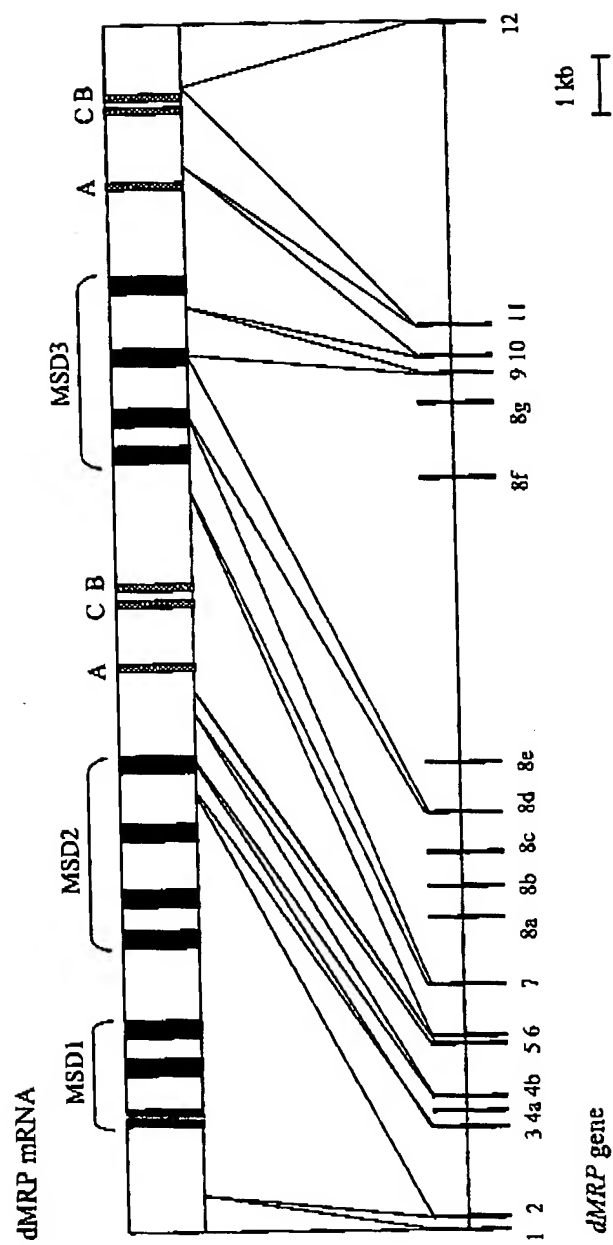


Figure 2

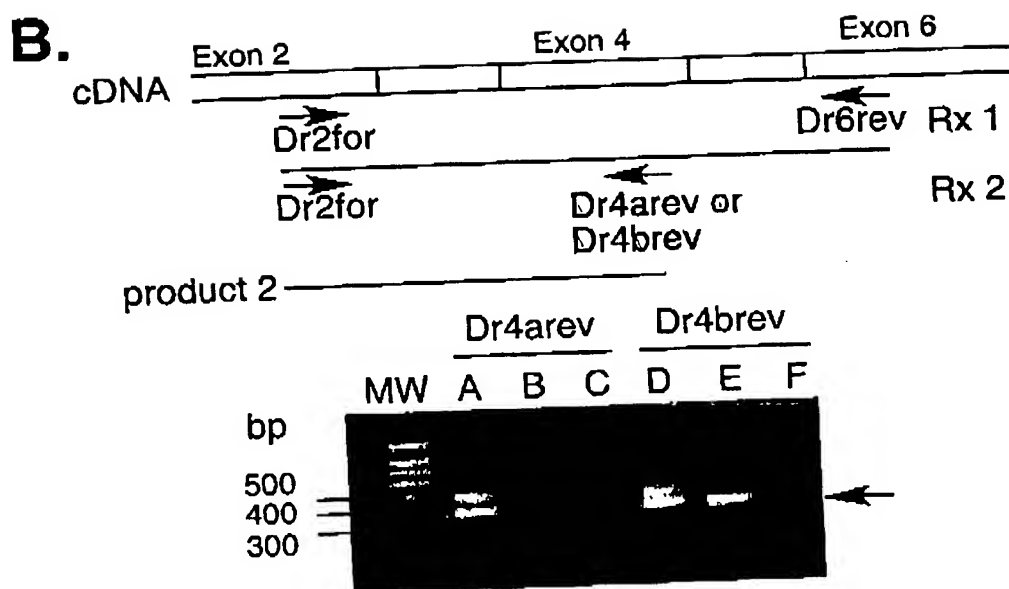
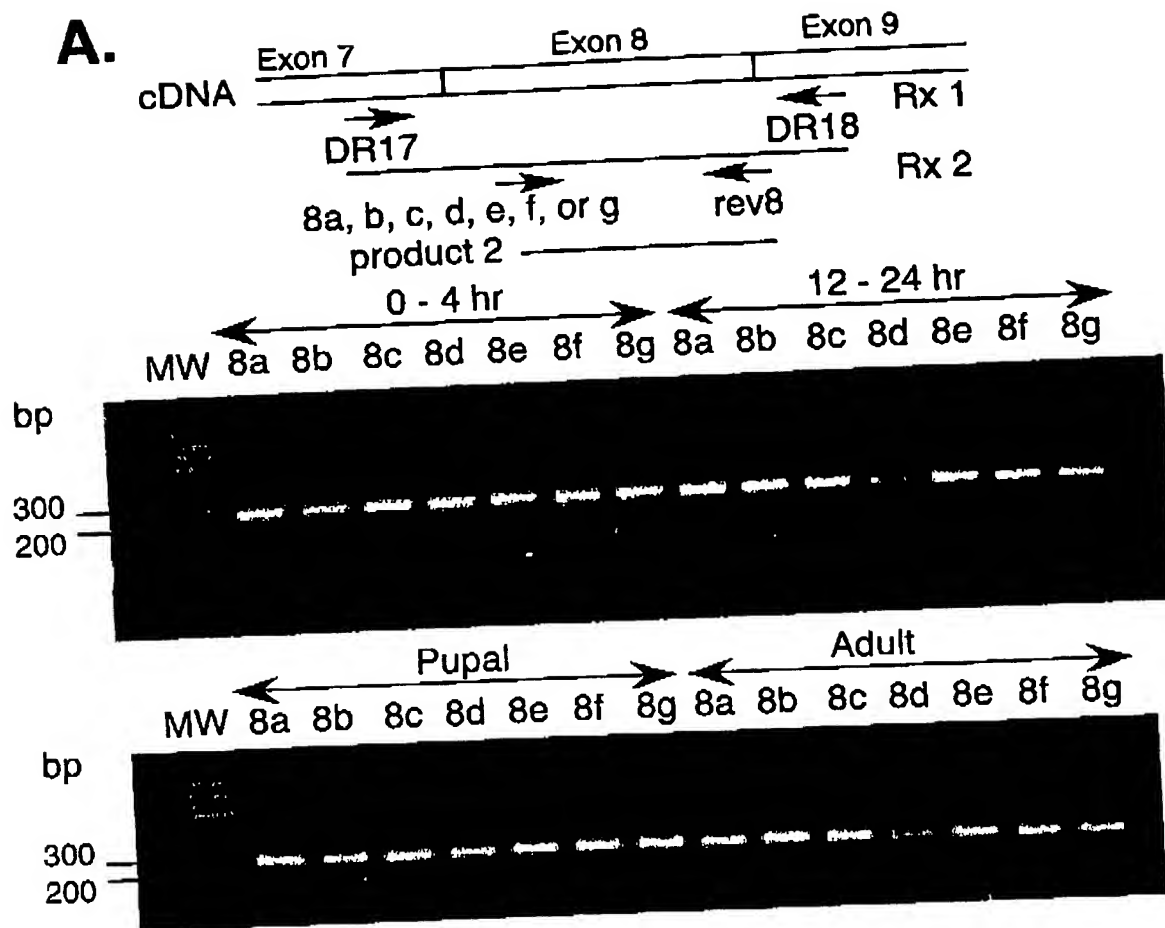


Figure 3

A

MRP1 VALCTFAVYVVTIDENN--ILDAQTAFAVSALFNILRFPNLNLPNVISSIVQ
 MRP2 VSVVTFVSVVLDVDSNN--ILDAQKAFSTITLNFILRFPNLNLPNVISSMLQ
 MRP3 VTLITLWVYVYVDPNN--VLDAAKAFVSLSLNFILRPLNMLPQLISNLTQ
 4a VSLVTFATYVLTSEAN--QLSVEKVLVSIALFDLMKLPILTILPMLSVDIAE
 4b VSLVTFATYVLTIDENN--VIDATXTFVSLSENLIRFRLTMLPMLITNLVQ
 Dsur ITPVTLGVYVNLHRDQEPDLNASRLFSLSALFQQLTVPLLIFFPITVPIIA
 Cons V-LVTFV-VYV--D-NN--LDA-K-FVS--LFNILR-PL--LPM-I-----Q

B

MRP1 IAVFGYSMAVSIGGILASRCLEKVDLLHSILR-SPMSFPFERTPSGNLVNRFPSKELDTVDSMIPEVIKMPMGSLFN
 MRP2 IFVFIARFWSAFGEVHASNIHLKQLLNNILR-APMRPFDTTPTGRIVNRFAGDISTVDDTLPOSLRSWITCFLG
 MRP3 FLVMLAAMAAAGGIQAARVLHQALJHNKIR-SPOSPFDTTTPSGRIILNCFPSKDIYVVDVLAQVILMLLNSPFN
 8a ATNFFSSLAISLGCCLKCSQLEQTLLYYNLR-WPMELFDITPLGRIVNRFPSKDIYVVDVLAQVILMLLNSPFN
 8b VTGYLSTLILSLGCVYSARYMHNVLHGTLR-WPMELFDITPLGRIVNRFPSKDIYVVDVLAQVILMLLNSPFN
 8c TSYYFCSTLALGCIPCSXLHETLSVVER-WPMELFDITPLGRIVNRFPSKDIYVVDVLAQVILMLLNSPFN
 8d LSKYLSGLALAIGGLHCSMNVFNNKLLNTGLK-WPMELFDITPLGRIVNRFPSKDIYVVDVLAQVILMLLNSPFN
 8e VLAYFAVVIIVYLGPFQAATIHNEELAVIIRGSVCRRFDTITPIGRLLNSPSCDMVDVDELPATMDSFMTPIFM
 8f LCNYGAAISLFTATLHASSRVFHRNFNNIMH-CPSEFFDTPPKGRILLDRCSDDVNCCLDLVMPNLNIRVMNSTAPQ
 8g PTSFSDLPALGSLHAAKVLHESMLLENVLR-APMTNFDITTPVGRILSRFSKDVSDQKMPQVINDCIWCAFE
 Dsur VSTPAGQYAGCNARRNLHDKLL(TILHKTLLH)-----FFQVTPPLGRIVNRFPSKDVSDQKMPQVINDCIWCAFE
 Pfam LLQGSFYUGERLQ-RLRKNLFALLRQILG-LFMSFFDTNSTGBLTSLTNDVSKINDGLGKGLLFQSLAT
 Cons -----G-----S--LH--LL--LR--PM-PFDTP-GRI-NRPSKD-----D--LP-----F--

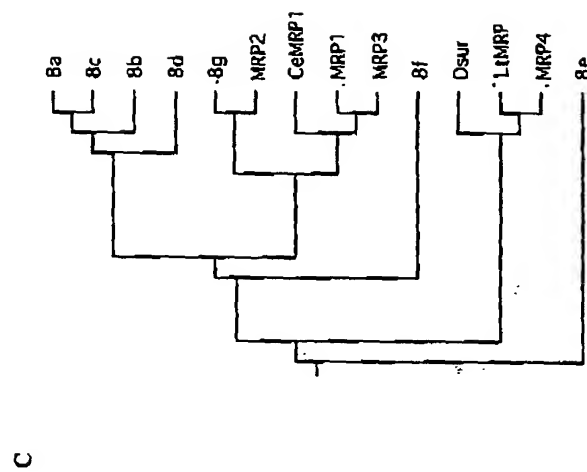


Figure 4

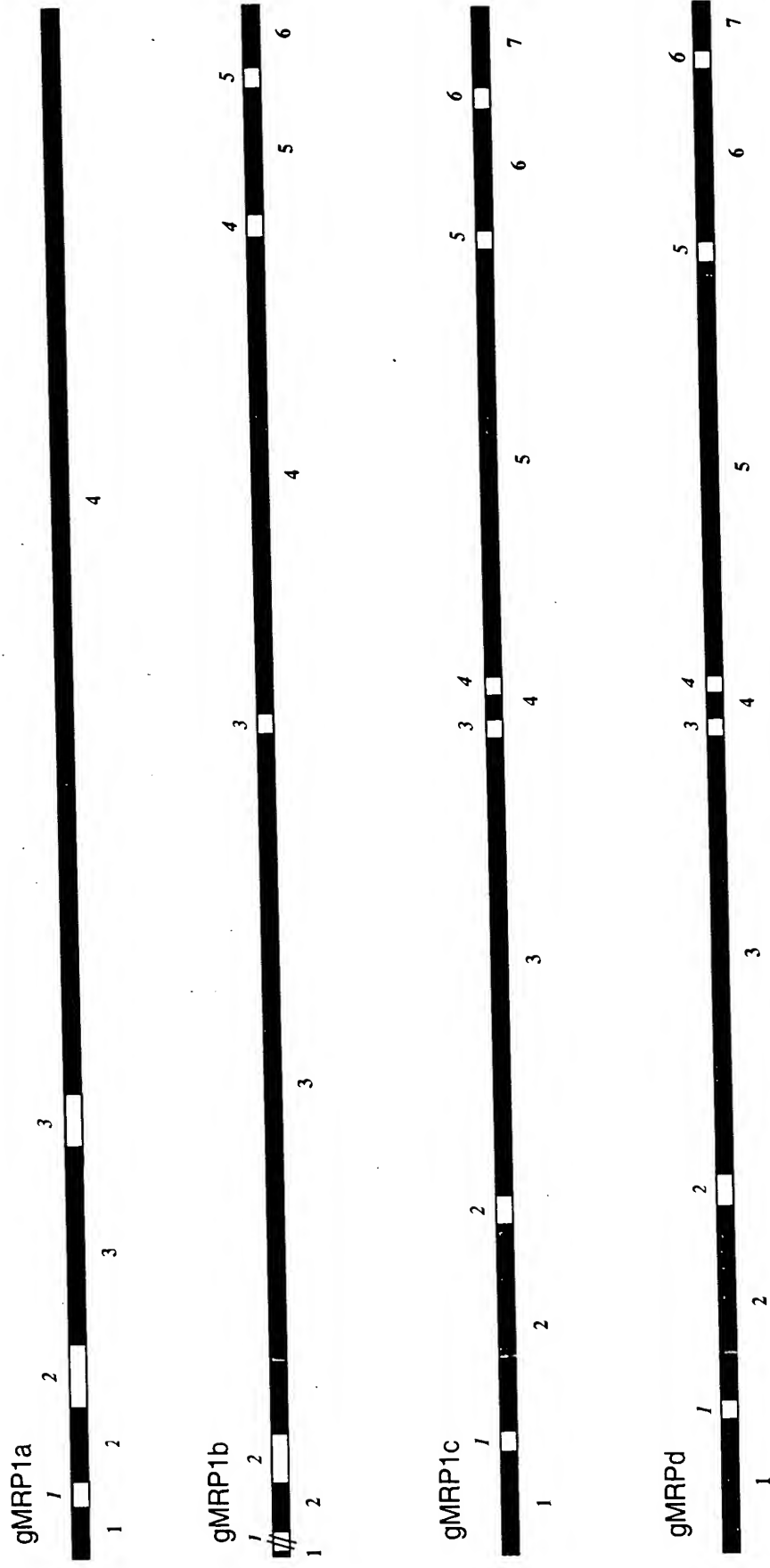


FIGURE 5

gMRP1c	MSD1	GEFVWDVNDNPNLTTCFCQRRVILQWVPCCLFLFVFVFSIYDI	50
gMRP1d		DEFFVWDVNDNPNLTTCFCQRRVILQWVPCCLFLFVFVFSIYDI	50
gMRP1b		DDLTWREEDPDLTTCFCQRRVILQWVPCCLFLFVFVFSIYDI	50
gMRP1a		DDLTWREEDPDLTTCFCQRRVILQWVPCCLFLFVFVFSIYDI	27
dMRP		ATEWYTNDPDMVEFVSLPLVDHLVVPVPCCLFLFVFVFSIYDI	58
MRP1		WNVNTSNDPDKCFQNTVLVWVPCCLFLFVFVFSIYDI	54
gMRP1c	MSD1	FLLMCMCWI DLGMVVGYYQ - - - DEQGLYDVQILTAVF	107
gMRP1d		FLLMCMCWI DLGMVVGYYQ - - - DEQGLYDVQILTAVF	107
gMRP1b		FLLMCMCWI DLGMVVGYYQ - - - DEQGLYDVQILTAVF	107
gMRP1a		FLLMCMCWI DLGMVVGYYQ - - - DEQGLYDVQILTAVF	82
dMRP		FLLMCMCWI DLGMVVGYYQ - - - DEQGLYDVQILTAVF	116
MRP1		FLLMCMCWI DLGMVVGYYQ - - - DEQGLYDVQILTAVF	112
gMRP1c	MSD1	FLLMCMCWI DLGMVVGYYQ - - - DEQGLYDVQILTAVF	168
gMRP1d		FLLMCMCWI DLGMVVGYYQ - - - DEQGLYDVQILTAVF	166
gMRP1b		FLLMCMCWI DLGMVVGYYQ - - - DEQGLYDVQILTAVF	161
gMRP1a		FLLMCMCWI DLGMVVGYYQ - - - DEQGLYDVQILTAVF	127
dMRP		FLLMCMCWI DLGMVVGYYQ - - - DEQGLYDVQILTAVF	176
MRP1		FLLMCMCWI DLGMVVGYYQ - - - DEQGLYDVQILTAVF	163
gMRP1c	MSD1	FLLMCMCWI DLGMVVGYYQ - - - DEQGLYDVQILTAVF	223
gMRP1d		FLLMCMCWI DLGMVVGYYQ - - - DEQGLYDVQILTAVF	223
gMRP1b		FLLMCMCWI DLGMVVGYYQ - - - DEQGLYDVQILTAVF	218
gMRP1a		FLLMCMCWI DLGMVVGYYQ - - - DEQGLYDVQILTAVF	174
dMRP		FLLMCMCWI DLGMVVGYYQ - - - DEQGLYDVQILTAVF	236
MRP1		FLLMCMCWI DLGMVVGYYQ - - - DEQGLYDVQILTAVF	220
gMRP1c	MSD2	FLLMCMCWI DLGMVVGYYQ - - - DEQGLYDVQILTAVF	274
gMRP1d		FLLMCMCWI DLGMVVGYYQ - - - DEQGLYDVQILTAVF	274
gMRP1b		FLLMCMCWI DLGMVVGYYQ - - - DEQGLYDVQILTAVF	269
gMRP1a		FLLMCMCWI DLGMVVGYYQ - - - DEQGLYDVQILTAVF	224
dMRP		FLLMCMCWI DLGMVVGYYQ - - - DEQGLYDVQILTAVF	287
MRP1		FLLMCMCWI DLGMVVGYYQ - - - DEQGLYDVQILTAVF	280
gMRP1c	MSD2	FLLMCMCWI DLGMVVGYYQ - - - DEQGLYDVQILTAVF	320
gMRP1d		FLLMCMCWI DLGMVVGYYQ - - - DEQGLYDVQILTAVF	320
gMRP1b		FLLMCMCWI DLGMVVGYYQ - - - DEQGLYDVQILTAVF	315
gMRP1a		FLLMCMCWI DLGMVVGYYQ - - - DEQGLYDVQILTAVF	263
dMRP		FLLMCMCWI DLGMVVGYYQ - - - DEQGLYDVQILTAVF	342
MRP1		FLLMCMCWI DLGMVVGYYQ - - - DEQGLYDVQILTAVF	334
gMRP1c	MSD2	FLLMCMCWI DLGMVVGYYQ - - - DEQGLYDVQILTAVF	378
gMRP1d		FLLMCMCWI DLGMVVGYYQ - - - DEQGLYDVQILTAVF	378
gMRP1b		FLLMCMCWI DLGMVVGYYQ - - - DEQGLYDVQILTAVF	373
gMRP1a		FLLMCMCWI DLGMVVGYYQ - - - DEQGLYDVQILTAVF	318
dMRP		FLLMCMCWI DLGMVVGYYQ - - - DEQGLYDVQILTAVF	402
MRP1		FLLMCMCWI DLGMVVGYYQ - - - DEQGLYDVQILTAVF	383

Figure 6

Figure 6

Figure 6

gMRP1c	B	ADAEVY	LFDD	PLSA	VD	AH	VG	KH	IF	EK	VI	IG	P	SG	ML	VG	KSR	LL	V	T	HG	I	S	F	L	P	F	V	E	N	I	L	V	L	K	821
gMRP1d		ADAEVY	LFDD	PLSA	VD	AH	VG	KH	IF	EK	VI	IG	P	SG	ML	VG	KSR	LL	V	T	HG	I	S	F	L	P	F	V	E	N	I	L	V	V	K	821
gMRP1b		ADAEVY	LFDD	PLSA	VD	AH	VG	KH	IF	EK	VI	IG	P	SG	ML	VG	KSR	LL	V	T	HG	I	S	F	L	P	F	V	E	N	I	L	V	V	K	816
gMRP1a		ADAEVY	LFDD	PLSA	VD	AH	VG	KH	IF	EK	VI	IG	P	SG	ML	VG	KSR	LL	V	T	HG	I	S	F	L	P	F	V	E	N	I	L	V	V	K	792
gMRP		ADAEVY	LFDD	PLSA	VD	AH	VG	KH	IF	EK	VI	IG	P	SG	ML	VG	KSR	LL	V	T	HG	I	S	F	L	P	F	V	E	N	I	L	V	V	K	845
MRP1		ADAEVY	LFDD	PLSA	VD	AH	VG	KH	IF	EK	VI	IG	P	SG	ML	VG	KSR	LL	V	T	HG	I	S	F	L	P	F	V	E	N	I	L	V	V	K	842
gMRP1c		DGEI	SE	SG	TY	QIE	LL	DQ	KG	AF	AE	FL	SQ	HI	QEL	DD	DE	DE	IE	IS	LI	QET	LL	ND	-	-	-	-	-	-	-	-	-	-	-	872
gMRP1d		DGEI	SE	SG	TY	QIE	LL	DQ	KG	AF	AE	FL	SQ	HI	QEL	DD	DE	DE	IE	IS	LI	QET	LL	ND	-	-	-	-	-	-	-	-	-	-	873	
gMRP1b		DGEV	SE	SG	TY	QIE	LL	DQ	KG	AF	AE	FL	SQ	HI	QEL	DD	DE	DE	IE	IS	LI	QET	LL	ND	-	-	-	-	-	-	-	-	-	-	888	
gMRP1a		GG	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	894			
gMRP		MGEI	SE	SG	TY	QIE	LL	VK	NG	KG	AF	AE	FL	SQ	HI	QEL	DD	DE	IE	IS	LI	QET	LL	ND	-	-	-	-	-	-	-	-	-	-	904	
MRP1		GGKI	SE	MG	SY	QIE	LL	AR	DG	AF	AE	FL	RT	YA	ST	EQ	EE	EE	EE	EE	EE	EE	EE	EE	-	-	-	-	-	-	-	-	-	893		
gMRP1c		NV	IQ	RA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	921		
gMRP1d		RIVER	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	923		
gMRP1b		KI	VQ	RA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	920		
gMRP1a		KAI	KL	AR	TES	LS	DS	I	SV	TS	AG	KL	QR	QL	SS	SS	SS	SS	SS	SS	SS	SS	SS	SS	-	-	-	-	-	-	-	-	-	-	841	
gMRP		KQ	ME	NG	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	983		
MRP1		IG	VE	ES	AT	GA	VT	WL	YK	KY	I	QS	IG	FK	FG	FG	SS	VL	FT	AI	IN	QG	SG	IF	SN	WL	LT	DW	SE	D	P	DA	AT	981		
gMRP1c		IE	KE	ES	AT	GA	VT	WL	YK	KY	I	QS	IG	FK	FG	FG	SS	VL	FT	AI	IN	QG	SG	IF	SN	WL	LT	DW	SE	D	P	DA	AT	983		
gMRP1d		IE	KE	ES	AT	GA	VT	WL	YK	KY	I	QS	IG	FK	FG	FG	SS	VL	FT	AI	IN	QG	SG	IF	SN	WL	LT	DW	SE	D	P	DA	AT	980		
gMRP1a		PK	GT	DH	GE	GN	VS	LG	LY	VT	FA	RM	LG	RR	Y	CV	GA	LC	FE	ST	VI	TA	LD	IV	IT	LL	QA	WA	AS	DK	QA	TS	901			
gMRP		IE	TE	KS	QT	GG	VE	FA	VY	KH	YI	KM	SA	IG	FL	SV	AT	LV	LF	FN	VF	QA	FD	IS	NY	WL	LT	QA	WA	AS	DK	QA	TS	1023		
MRP1		ME	AD	KA	QT	GG	VE	FA	VY	KH	YI	KM	SA	IG	FL	SV	AT	LV	LF	FN	VF	QA	FD	IS	NY	WL	LT	QA	WA	AS	DK	QA	TS	1007		
gMRP1c		DP	SV	RD	KY	LG	VY	GA	LG	GA	QS	IA	LF	VA	AL	LS	LG	CL	KA	AK	EE	SH	KN	KL	LE	SC	LR	MP	MS	FF	DT	TT	1041			
gMRP1d		DT	SV	RD	KY	LG	VY	GA	LG	GA	QS	IA	LF	VA	AL	LS	LG	CL	KA	AK	EE	SH	KN	KL	LE	SC	LR	MP	MS	FF	DT	TT	1043			
gMRP1b		DT	SV	RD	KY	LG	VY	GA	LG	GA	QS	IA	LF	VA	AL	LS	LG	CL	KA	AK	EE	SH	KN	KL	LE	SC	LR	MP	MS	FF	DT	TT	1040			
gMRP1a		GA	LL	HT	TT	WI	LC	VW	VL	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	955			
gMRP		DT	GL	RD	KY	LG	VY	GA	LG	GA	QS	IA	LF	VA	AL	LS	LG	CL	KA	AK	EE	SH	KN	KL	LE	SC	LR	MP	MS	FF	DT	TT	1089			
MRP1		TQ	EH	TK	VR	LS	VY	GA	LG	GA	QS	IA	LF	VA	AL	LS	LG	CL	KA	AK	EE	SH	KN	KL	LE	SC	LR	MP	MS	FF	DT	TT	1067			
gMRP1c		PL	GR	I	IN	RF	SK	DV	VD	VN	VL	PA	VT	IR	AW	LL	FL	FN	V	FG	VF	VI	IG	TS	TP	IF	LA	V	VP	PL	MI	Y	Y	1101		
gMRP1d		PL	GR	I	IN	RF	SK	DV	VD	VN	VL	PA	VT	IR	AW	LL	FL	FN	V	FG	VF	VI	IG	TS	TP	IF	LA	V	VP	PL	MI	Y	Y	1103		
gMRP1b		PL	GR	I	IN	RF	SK	DV	VD	VN	VL	PA	VT	IR	AW	LL	FL	FN	V	FG	VF	VI	IG	TS	TP	IF	LA	V	VP	PL	MI	Y	Y	1100		
gMRP1a		PL	GR	I	IN	RF	SK	DV	VD	VN	VL	PA	VT	IR	AW	LL	FL	FN	V	FG	VF	VI	IG	TS	TP	IF	LA	V	VP	PL	MI	Y	Y	1015		
gMRP		PS	GN	LV	NR	FS	KE	LD	TV	DS	MI	PE	VI	KM	FM	GS	LF	FN	V	FG	VF	VI	IG	TS	TP	IF	LA	V	VP	PL	MI	Y	Y	1143		
MRP1		FV	QR	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1127			
gMRP1c		FV	QR	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1154			
gMRP1d		LI	QK	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1156			
gMRP1b		ML	VC	GL	KR	LL	SY	HL	QV	AR	TL	KR	FE	AS	SR	SP	PI	Y	SH	FE	SE	TS	IR	AY	GA	QQ	DR	FM	NE	SE	EH	Q	1153			
gMRP1a		FA	QR	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1075			
gMRP		FV	QR	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1198			
MRP1		FV	QR	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1180			

Figure 6

gMRP1c	R	V	D	Y	N	Q	L	V	S	Y	P	T	I	V	A	N	R	W	L	A	V	R	L	E	I	G	S	C	V	I	L	F	A	A	L	F	A	I	L	A	R	D	T	I	G	Q	A	T	V	G	V	S	I	S	Y	A	L	Q	I	1214																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								
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Figure 6